

- 1 -

SEQUENCE LISTING

<110> Bayer AG, BHC

<120> Diagnostics and Therapeutics for Diseases Associated with Arginyl Aminopeptidase RNPEP-like (RNPEP-like)

<130> Le A 36 900

<160> 5

<170> PatentIn version 3.1

<210> 1

<211> 3527

<212> DNA

<213> Homo sapiens

<400> 1

agtaaccccg agtctgcgga agtggtgacc cgtgggacgc ggctgagaca ggagactgaa	60
aggaaccata atttgtgaca tcagttgttt tctttgataa gcagctattt atgattctgg	120
aagattaagg cagataggaa accccatctg agatttaat aaatccctca aacaataaac	180
cacatcatgg acatacagct ggacccctgcc agagatgacc tgcctctcat gcccaacacc	240
agccacatac ttgtgaagca ctatgtactg gatttggatg tggatttga aagtcaagtc	300
attgagggga ccatagtgct tttcctcgag gatggaaaca gattcaagaa acagaatagc	360
tctattgagg aagcctgccca atcagaatca aacaaagcct gcaaatttgg gatgcctgaa	420
ccctgccata ttcccggtac aaatgcaagg accttctcat ctgaaatgga atataatgat	480
tttgcaatct gtagtaaagg tgaaaaagat acttctgata aagatggtaa ccatgacaac	540
caggaacatg cttctggat ttctagctca aagtactgct gtgacacagg gaatcatggg	600
agtgaggatt ttttcttagt gttggactgc tggatttat ctgtgttaaa agtcgaggag	660
gtggatgttg ctgctgtgcc aggtctggaa aaatttacaa ggtctcctga gtcacgggt	720
gtttctgagg agttcaggaa tcagattgta cgtgaacttg tgactttgcc tgcaaatcg	780
tggagggagc agtttagacta ttacgctcgc tgcagccagg ctccctggctg tggggaaactc	840
ctctttgaca ctgacacttg gagcttgcag ataaggaaga cagggctca gacagctact	900
gactttccctc atgctatcag gatatggtac aaaactaaac ctgaagggcg atcggttaca	960
tggacctcag accagagtgg caggccatgt gtttatactg tggatctcc cataaacaac	1020
aggccccttt ttccatgccca ggagccaccc gttgccatgt caacatggca ggctacagtt	1080
cgagcagctg catctttgt tggatggaaa attctccaa accaacgcag	1140
ctttggaaag agtgctcaag ctggattac tatgtacta tgccaatgcc agcctccacc	1200
ttcacaattg cagtggatg ctggacagaa atgaagatgg agacatggtc atcaaatgat	1260
ttggcaacag agagacccctt ctcacccctt gaggccaaact tcaggcatgt tggatggat	1320
agtcacatgg aataacccctg ccgcttccag aatgcttctg ccaccaccca ggagatcatt	1380
cctcatcggtt tctttgcccc tggatggatc acgggtgcctt gccaagagac cttctgcgg	1440

- 2 -

ctgatccctc	cttgcccttc	agcagcacat	tctgttctgg	gagcacacccc	gttctctcgg	1500
ctggatgttc	tcatcgcccc	tgccaaacttt	ccaagtctgg	ggatggccag	cccacacatc	1560
atgttccctc	ctcagagcat	cttgacagga	ggaaaccatc	tctgtgggac	ccgcctctgc	1620
catgaaattg	cccatgcctg	gtttggccta	gccatcgggg	cccgagactg	gacggaggag	1680
tggctgagtg	aaggcttcgc	cactcacttg	gaggatgtgt	tttggccac	agcacagcag	1740
ctggccccc	atgaggcccc	ggagcagcag	gagctgaggg	cttgcgtgcg	ctggcgctgc	1800
ctccaggacg	agatgcaatg	ctcccccgag	gagatgcagg	tgttaagggtt	tccacatgtt	1860
ggcggatgca	gtggaaagtt	ctctgagat	ctttgccaca	ctgttcaaca	tgtttgacca	1920
ctctgtccct	aaaacgcctt	cttcattaaag	cactttctcc	tcctggcctt	cctgagcttc	1980
ttccggagc	tgaaggagca	gagcgtggac	tgccggggcag	ggctggaatt	cgagcgctgg	2040
ctcaatgcca	caggcccccc	gctggctgag	ccggaccctgt	ctcagggatc	cagcctgacc	2100
cggcccgctgg	aggccctttt	ccagctgtgg	accgcagaac	ctctggacca	ggcagctgcc	2160
tccggccagcg	ccattgacat	ctccaaagtgg	aggacccttc	agacagcaact	cttccctggac	2220
cggttcctgg	atgggtcccc	gtgcccag	gaggtgggtga	tgagcctgtc	caagtgtac	2280
tcctccctgc	tggactcgat	gaacgctgag	atccgcatcc	gtcggctgca	gattgaggtc	2340
cgcaacact	actatccatg	cctccacagg	gtgcggcgct	tcctggagag	ccagatgtca	2400
cgcatgtaca	ccatcccgt	gtacgaggac	cttcgcacccg	gtgcctcaa	gtccttcgct	2460
ctggaggtct	tctaccagac	gcagggccgg	ctgcacccca	acctgcgcag	agccatccag	2520
cagatcctgt	cccagggcct	gggctccagc	acagagcccc	cctcagagcc	cagcacggag	2580
ctgggcaagg	ctgaagcaga	cacagactcg	gacgcacagg	ccctgctgt	tggggacgag	2640
gccccccagca	gtgccatctc	tctcaggac	gtcaatgtgt	ctgcctagcc	ctgttggcgg	2700
gctgaccctc	gaccccacag	acaccacaat	tgtgccttct	gtggccagg	cctgccatga	2760
ctgcgtctcg	gctctggcca	tgagctctgc	ccaggccac	aagccctcc	cctgggctct	2820
cccaggcagg	gagaatgggg	agagggacct	ccttgcgtct	ggcagagacc	tgtggacctg	2880
gcctccccac	tcccagctct	cttgcactgc	aggccc	tggg	gccagcccgc	2940
ccteetgtct	caacactgac	agctgtgcct	agccccggat	gccagcacct	gccaggtgcc	3000
gccccggggc	aaggccccca	gcagccctat	ggtgac	ccgc	acactgtgcc	3060
ccggggggccc	aggctgtgt	gtccctgcag	cacgcctcc	tgcagggatc	tgagccaccc	3120
tccccgcaca	gcctgcacc	ccgc	ggttggcagc	ctcagttgc	ccctggcaga	3180
ggaacaagga	cacagacatt	ccctcagtgt	ggggggcagg	ggacacaggg	agaggatgg	3240
tgtccctggg	gagggccctc	tggcccagg	caaccttage	ccctcagaac	agggagtccc	3300
aggacccagg	gagagtgtgg	ggacaggaca	gcctgtctct	tgtagcttcc	tggggtgaaa	3360
ggcacagggg	caaagcaata	ccccaggaa	agtggaggt	ggtgctggtg	ctctctccag	3420
gcccaccatg	ctgggagagg	cgccagac	ctggggcctc	cagcctggga	ctgctgtgat	3480
ggggtatcac	ggtgatggtc	ccattaaact	tccact	ctgc	aaacctg	3527

<210> 2

<211> 566

<212> PRT

<213> Homo sapiens

<400> 2

Met Asp Ile Gln Leu Asp Pro Ala Arg Asp Asp Leu Pro Leu Met Ala

- 3 -

1	5	10	15
Asn Thr Ser His Ile Leu Val Lys His Tyr Val Leu Asp Leu Asp Val			
20	25	30	
Asp Phe Glu Ser Gln Val Ile Glu Gly Thr Ile Val Leu Phe Leu Glu			
35	40	45	
Asp Gly Asn Arg Phe Lys Lys Gln Asn Ser Ser Ile Glu Glu Ala Cys			
50	55	60	
Gln Ser Glu Ser Asn Lys Ala Cys Lys Phe Gly Met Pro Glu Pro Cys			
65	70	75	80
His Ile Pro Val Thr Asn Ala Arg Thr Phe Ser Ser Glu Met Glu Tyr			
85	90	95	
Asn Asp Phe Ala Ile Cys Ser Lys Gly Glu Lys Asp Thr Ser Asp Lys			
100	105	110	
Asp Gly Asn His Asp Asn Gln Glu His Ala Ser Gly Ile Ser Ser Ser			
115	120	125	
Lys Tyr Cys Cys Asp Thr Gly Asn His Gly Ser Glu Asp Phe Leu Leu			
130	135	140	
Val Leu Asp Cys Cys Asp Leu Ser Val Leu Lys Val Glu Glu Val Asp			
145	150	155	160
Val Ala Ala Val Pro Gly Leu Glu Lys Phe Thr Arg Ser Pro Glu Leu			
165	170	175	
Thr Val Val Ser Glu Glu Phe Arg Asn Gln Ile Val Arg Glu Leu Val			
180	185	190	
Thr Leu Pro Ala Asn Arg Trp Arg Glu Gln Leu Asp Tyr Tyr Ala Arg			
195	200	205	
Cys Ser Gln Ala Pro Gly Cys Gly Glu Leu Leu Phe Asp Thr Asp Thr			
210	215	220	
Trp Ser Leu Gln Ile Arg Lys Thr Gly Ala Gln Thr Ala Thr Asp Phe			
225	230	235	240
Pro His Ala Ile Arg Ile Trp Tyr Lys Thr Lys Pro Glu Gly Arg Ser			
245	250	255	
Val Thr Trp Thr Ser Asp Gln Ser Gly Arg Pro Cys Val Tyr Thr Val			
260	265	270	
Gly Ser Pro Ile Asn Asn Arg Ala Leu Phe Pro Cys Gln Glu Pro Pro			
275	280	285	
Val Ala Met Ser Thr Trp Gln Ala Thr Val Arg Ala Ala Ala Ser Phe			
290	295	300	
Val Val Leu Met Ser Gly Glu Asn Ser Ala Lys Pro Thr Gln Leu Trp			
305	310	315	320
Glu Glu Cys Ser Ser Trp Tyr Tyr Val Thr Met Pro Met Pro Ala			
325	330	335	
Ser Thr Phe Thr Ile Ala Val Gly Cys Trp Thr Glu Met Lys Met Glu			
340	345	350	

- 4 -

Thr Trp Ser Ser Asn Asp Leu Ala Thr Glu Arg Pro Phe Ser Pro Ser
 355 360 365
 Glu Ala Asn Phe Arg His Val Gly Val Cys Ser His Met Glu Tyr Pro
 370 375 380
 Cys Arg Phe Gln Asn Ala Ser Ala Thr Thr Gln Glu Ile Ile Pro His
 385 390 395 400
 Arg Val Phe Ala Pro Val Cys Leu Thr Gly Ala Cys Gln Glu Thr Leu
 405 410 415
 Leu Arg Leu Ile Pro Pro Cys Leu Ser Ala Ala His Ser Val Leu Gly
 420 425 430
 Ala His Pro Phe Ser Arg Leu Asp Val Leu Ile Val Pro Ala Asn Phe
 435 440 445
 Pro Ser Leu Gly Met Ala Ser Pro His Ile Met Phe Leu Ser Gln Ser
 450 455 460
 Ile Leu Thr Gly Gly Asn His Leu Cys Gly Thr Arg Leu Cys His Glu
 465 470 475 480
 Ile Ala His Ala Trp Phe Gly Leu Ala Ile Gly Ala Arg Asp Trp Thr
 485 490 495
 Glu Glu Trp Leu Ser Glu Gly Phe Ala Thr His Leu Glu Asp Val Phe
 500 505 510
 Trp Ala Thr Ala Gln Gln Leu Ala Pro Tyr Glu Ala Arg Glu Gln Gln
 515 520 525
 Glu Leu Arg Ala Cys Leu Arg Trp Arg Arg Leu Gln Asp Glu Met Gln
 530 535 540
 Cys Ser Pro Glu Glu Met Gln Val Leu Arg Phe Pro His Val Gly Gly
 545 550 555 560
 Cys Ser Gly Ser Phe Ser
 565

<210> 3
 <211> 20
 <212> DNA
 <213> artificial sequence

<220>
 <223> forward primer

<400> 3
 ccaggacgag atgcaatgct

<210> 4
 <211> 18
 <212> DNA

- 5 -

<213> artificial sequence

<220>

<223> reverse primer

<400> 4

tgcatccgcc aacatgtg

18

<210> 5

<211> 25

<212> DNA

<213> artificial sequence

<220>

<223> probe

<400> 5

cgaggaga~~t~~g caggtgttaa gg~~t~~tt

25